AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1-9. (Canceled)

10. (Withdrawn) A computer-implemented method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:

(a) providing X, Y and Z atomic structure coordinates set forth in any of figures 7-304 for all or a portion of an HPTPbeta catalytic domain [SEQ ID NO:7];

(b) determining a three-dimensional structure of all or a portion of an HPTPbeta catalytic domain [SEQ ID NO:7] from said X, Y and Z coordinates;

(c) imaging said three-dimensional structure of all or a portion of an HPTPbeta catalytic domain [SEQ ID NO:7];

(d) positioning one or more candidate compounds at one or more areas of said imaged three-dimensional structure by using binding modes(s) of said one or more candidate compounds with said area(s) of said imaged three-dimensional structure; and

(e) identifying from said one or more candidate compounds those that bind or modulate HPTPbeta as drug candidate compounds useful for the treatment of an angiogenesis mediated disorder.

11. (Withdrawn) The method of claim 10, further comprising determining the one or more locations or binding geometries of said positioned one or more candidate compounds relative to any of said X, Y and Z atomic structure coordinates.

12. (Withdrawn) The method of claim 10, further comprising assembling fragments of said one or more candidate compounds together to create an assembled compound.

13. (Withdrawn) The method of claim 12, further comprising analyzing the ability of said assembled compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

14. (Withdrawn) The method of claim 10, wherein said one or more candidate compounds or portion(s) thereof are HPTPbeta agonists.

15. (Withdrawn) The method of claim 14, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

16. (Withdrawn) The method of claim 10, wherein said one or more candidate compounds or portion(s) thereof are HPTPbeta antagonists.

17. (Withdrawn) The method of claim 16, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

18. (Withdrawn) The method of claim 10, wherein said X, Y and Z atomic structure coordinates of said three-dimensional structure are HPTPbeta binding sites or combinations thereof.

19. (Withdrawn) The method of claim 10, wherein said one or more candidate compounds are positioned at at least one of the P(0), P(+1) and P(-1) binding sites of HPTPbeta.

20. (Withdrawn) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290, and 293 of SEQ ID NO:7.

21. (Withdrawn) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO:7.

22. (Withdrawn) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 69-76, 119-123, and 149-154 of SEQ ID NO:7.

23. (Withdrawn) The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain [SEQ ID NO:7] has unit cell dimensions of approximately a=39Å, b=72 Å, c=120 Å, $\alpha=90^{o}$, $\beta=90^{o}$, $\gamma=90^{o}$ in the space group $P2_12_12_1$.

24. (Withdrawn) The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain [SEQ ID NO:7] has unit cell dimensions of approximately a=62Å, b=72 Å, c=70 Å, $\alpha=90^{o}$, $\beta=93^{o}$, $\gamma=90^{o}$ in the space group $P2_1$.

25. (Currently Amended) A method of identifying a drug candidate compound for the treatment of an angiogenic mediated disorder, comprising:

a) ~~imaging, through the use of computer modeling of X, Y and Z atomic structure~~ employing the three-dimensional structural coordinates ~~set forth in Figures 202-252, an~~ of the HPTPbeta catalytic domain [SEQ ID NO:7] as set forth in Figures 202-252 to graphically image the HPTPbeta catalytic domain [SEQ ID NO:7], and determining the binding mode of a compound within the catalytic domain;

b) selecting one or more compounds which have similar binding modes with the HPTPbeta catalytic domain [SEQ ID NO:7] as set forth in Figures 202-252 wherein the compounds are computationally positioned ~~positioning a drug candidate compound~~ at one or more areas of said imaged HPTPbeta catalytic domain [SEQ ID NO:7] ~~by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain~~; and

c) assaying ~~analyzing~~ the ability of said drug candidate compound to bind or modulate HPTPbeta activity ~~in an *in vivo* or *in vitro* assay~~.

26. (Currently Amended) A method of identifying a drug candidate compound for the treatment of an angiogenic mediated disorder, comprising:

a) ~~imaging, through the use of computer modeling of X, Y and Z~~ ~~atomic structure~~ employing the three-dimensional structural coordinates ~~set forth in Figures 7-102, an~~ of the HPTPbeta catalytic domain [SEQ ID NO:7] as set forth in Figures 7-102 to graphically image the HPTPbeta catalytic domain [SEQ ID NO:7], and determining the binding mode of a compound within the catalytic domain;

b) selecting one or more compounds which have similar binding modes with the HPTPbeta catalytic domain [SEQ ID NO:7] as set forth in Figures 7-102 wherein the compounds are computationally positioned ~~positioning a drug candidate compound~~ at one or more areas of said imaged HPTPbeta catalytic domain [SEQ ID NO:7] ~~by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain~~; and

c) assaying ~~analyzing~~ the ability of said drug candidate compound to bind or modulate HPTPbeta activity ~~in an *in vivo* or *in vitro* assay~~.

27. (Previously Presented) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290, and 293 of [SEQ ID NO:7].

28. (Previously Presented) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290, and 293 of [SEQ ID NO:7].

29. (Previously Presented) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of [SEQ ID NO:7].

30. (Previously Presented) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of [SEQ ID NO:7].

31. (Previously Presented) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123, and 149-154 of [SEQ ID NO:7].

32. (Previously Presented) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123, and 149-154 of [SEQ ID NO:7].

33. (New) A method of identifying an inhibitor of an HPTPbeta molecule, comprising:

a) providing a crystal of HPTPbeta comprising the amino acid residues of [SEQ ID NO:7];

b) determining the three-dimensional atomic coordinates of amino acids Asn74 Asn75 Ile76, Leu77, Cys152, Pro209, Asp210, His211, Gly212, Val213, Pro214, Cys244, Ser245, Ala246, Gly247, Val248, Gly249, Arg250, Thr251, Gly252, Thr253, Gln288, Thr289, Glu290, and Tyr293 of an active binding site of the HPTPbeta molecule by X-ray diffraction of the crystal;

c) using the atomic coordinates of amino acids Asn74 Asn75 Ile76, Leu77, Cys152, Pro209, Asp210, His211, Gly212, Val213, Pro214, Cys244, Ser245, Ala246, Gly247, Val248, Gly249, Arg250, Thr251, Gly252, Thr253, Gln288, Thr289, Glu290, and Tyr293 so that the root mean square deviation of conserved residue backbone atoms is less than 1.5 Å, to generate a three-dimensional structure of a molecule comprising an HPTPbeta active site binding pocket;

d) employing the three-dimensional structure to design or select a potential drug candidate; and

e) contacting the potential drug candidate with the molecule to determine the ability of the potential inhibitor to associate with the molecule.

34. (New) A method of identifying an inhibitor of an HPTPbeta molecule, comprising:

a) using the structure coordinates of HPTPbeta [SEQ ID NO:7] so that the root mean square deviation of conserved residue backbone atoms is less than 1.5 Å, to generate a three-dimensional structure of a molecular complex comprising an

active site binding pocket of amino acids residues Asn74 Asn75 Ile76, Leu77, Cys152, Pro209, Asp210, His211, Gly212, Val213, Pro214, Cys244, Ser245, Ala246, Gly247, Val248, Gly249, Arg250, Thr251, Gly252, Thr253, Gln288, Thr289, Glu290, and Tyr293 wherein the binding site is a binding site for HPTPbeta [SEQ ID NO:7];

b) employing the three-dimensional structure to design or select a potential drug candidate;

c) synthesizing the potential drug candidate; and

d) contacting the potential drug candidate with the molecule to determine the ability of the potential inhibitor to associate with HPTPbeta [SEQ ID NO:7].

35. (New) A method of identifying an inhibitor of an HPTPbeta molecule, comprising:

a) providing a crystal of HPTPbeta comprising the amino acid residues of [SEQ ID NO:7];

b) determining the three-dimensional atomic coordinates of amino acids Glu48, Glu49, Leu50, Lys51, Asp52, Val53, Gly54, Arg55, Asn56, Gln57, Ser58, Cys59, Asp60, Ile61, Ala62, Leu63, Leu64, Pro65, Glu66, Ile76, Leu77, Pro78, Tyr79, Asp80, Gly212, Val213, Pro214, Val284, His285, Met286, Val287, Gln288, Thr289, Glu290, Cys291, and Gln292 of an active binding site of the HPTPbeta molecule by X-ray diffraction of the crystal;

c) using the atomic coordinates of amino acids Glu48, Glu49, Leu50, Lys51, Asp52, Val53, Gly54, Arg55, Asn56, Gln57, Ser58, Cys59, Asp60, Ile61, Ala62, Leu63, Leu64, Pro65, Glu66, Ile76, Leu77, Pro78, Tyr79, Asp80, Gly212, Val213, Pro214, Val284, His285, Met286, Val287, Gln288, Thr289, Glu290, Cys291, and Gln292 so that the root mean square deviation of conserved residue backbone atoms is less than 1.5 Å, to generate a three-dimensional structure of a molecule comprising an HPTPbeta active site binding pocket;

d) employing the three-dimensional structure to design or select a potential drug candidate; and

e) contacting the potential drug candidate with the molecule to determine the ability of the potential inhibitor to associate with the molecule.

36. (New) A method of identifying an inhibitor of an HPTPbeta molecule, comprising:

a) using the structure coordinates of HPTPbeta [SEQ ID NO:7] so that the root mean square deviation of conserved residue backbone atoms is less than 1.5 Å, to generate a three-dimensional structure of a molecular complex comprising an active site binding pocket of amino acids residues Glu48, Glu49, Leu50, Lys51, Asp52, Val53, Gly54, Arg55, Asn56, Gln57, Ser58, Cys59, Asp60, Ile61, Ala62, Leu63, Leu64, Pro65, Glu66, Ile76, Leu77, Pro78, Tyr79, Asp80, Gly212, Val213, Pro214, Val284, His285, Met286, Val287, Gln288, Thr289, Glu290, Cys291, and Gln292 wherein the binding site is a binding site for HPTPbeta [SEQ ID NO:7];

b) employing the three-dimensional structure to design or select a potential drug candidate;

c) synthesizing the potential drug candidate; and

d) contacting the potential drug candidate with the molecule to determine the ability of the potential inhibitor to associate with HPTPbeta [SEQ ID NO:7].